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赤潮期間中囲まれた湾でメタバーコーディングを使って二つのメガウイルス科群集の比較
Comparing two Megaviridae communities using meta-barcode during a red tide period in an enclosed bay

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研究成果概要

This study is using the supercomputer of Institute for Chemical Research, Kyoto University, to do an analysis for comparing two Megaviridae communities during a red tide period in an enclosed bay, west Japan.

“Megaviridae” is a proposed family of giant viruses infecting unicellular eukaryotes. They are very abundant and ubiquitous in the sea water and affect marine microbial community by their lytic infection cycle. However, only a few Megaviridae members have been explored in the marine environments, and their ecological roles in marine ecosystems remains unknow.

For studying the differences of Megaviridae community in two different kind of water, surface sea water samples (0.22-3 μm) were collected from an enclosed bay (Uranouchi Inret, Kochi) during a red tide period. A set of degenerated primers (called “MEGAPRIMER”), which target family B DNA polymerase genes of Megaviridae, was used to assess the composition of Megaviridae community. Bioinformatic analysis was applied after sequencing. As a result, hundreds of operational taxonomic units (OTUs) were identified in each sample. When we compared the Megaviridae structures between within and without red-tide waters, there was a clear difference between these two samples in a community variation analysis. The difference was also visible in dominant OTU proportions between the two types of samples. Phylogenetic analysis based on a maximum-likelihood method showed that almost all of the OTUs belong to unknown Megaviridae branches. Future study will mainly focus on the host-virus interactions and the relationship between viral community and environmental factors, that may reveal ecological functions of Megaviridae in a coastal ecosystem.

発表論文（謝辞あり）

発表論文（謝辞なし）